

National Library
of Medicine

PubMed

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search PubMed	▼	for					Go	Clear
Limits		Preview/Index		History		Clipboard		

Entrez PubMed

☐ 1: *Virology* 1990 May;176(1):114-25[Related Articles](#), [Books](#), [Protein](#), [Nucleotide](#),
[LinkOut](#)

PubMed Services

Coding properties of the S and the M genome segments of Sapporo rat virus: comparison to other causative agents of hemorrhagic fever with renal syndrome.**Arikawa J, Lapenotiere HF, Iacono-Connors L, Wang ML, Schmaljohn CS**

Related Resources

Virology Division, United States Army Medical Research Institute of Infectious Diseases, Fort Detrick, Frederick, Maryland 21701-5011.

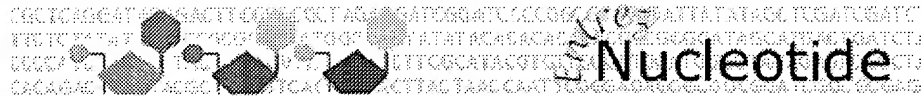
Three serologically distinct groups of hantaviruses have been associated with severe, moderate, and mild forms of hemorrhagic fever with renal syndrome (HFRS). To gain a better understanding of the genetic variation among these viruses, we cloned and sequenced the M and the S genome segments of Sapporo rat virus, an etiologic agent of moderate HFRS, and compared the predicted gene products to those of Hantaan virus, and the Hallnas strain of Puumala virus, which are etiologic agents of severe and mild HFRS, respectively. The SR-11 S segment consisted of 1769 nucleotides and had an open reading frame (ORF) in the virus-complementary sense RNA with a coding capacity of 429 amino acids. Deduced amino acids from the SR-11 S segment ORF displayed 83% homology with those of Hantaan nucleocapsid (N) protein. Comparison of the S segment ORFs of all three viruses revealed 58% homology. No evidence for additional nonstructural protein(s) encoded by the SR-11 S segment was obtained. The SR-11 M segment consisted of 3651 nucleotides and had an ORF in the virus-complementary sense RNA with a coding capacity of 1134 amino acids. Amino acid sequences predicted from the SR-11 M segment ORF were 75% homologous with those encoding Hantaan G1 and G2 envelope glycoproteins. Comparison of the deduced amino acid sequences of the M segment ORFs of SR-11, Hantaan, and Hallnas viruses revealed a 43% homology for amino acids constituting the G1 proteins and a 55% homology for amino acids constituting the G2 proteins of the three viruses. The envelope proteins of SR-11 virus were localized within the M segment ORF by amino-terminal sequence analysis of purified G1 and G2. G1 initiated at amino acid 17 and G2 at amino acid 647 within the ORF. Five potential asparagine-linked glycosylation sites were

identified in the SR-11 G1 coding sequences, four of which were conserved between Hantaan and SR-11 viruses and three of which were conserved among all three viruses. One potential glycosylation site was identified in the SR-11 G2 coding sequences and was conserved among Hantaan, SR-11 and Hallnas viruses. Cysteine residues were highly conserved within the M segment ORFs of all three viruses, suggesting a similar structure and function of the G1 and G2 proteins.

PMID: 1970443

Display	Abstract	<input type="button" value="v"/>	Save	Text	Order	Add to Clipboard
---------	----------	----------------------------------	------	------	-------	------------------

[Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)
[Department of Health & Human Services](#)
[Freedom of Information Act](#) | [Disclaimer](#)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search		Nucleotide	for			Go	Clear
Limits		Index		History		Clipboard	
Display	Default View	as	HTML	Save	Add to Clipboard		

☐ 1: **M34882 Sapporo rat virus mRNA M segment, encoding an ORF, complete cds** PubMed, Protein, Related Sequences, Taxonomy

LOCUS SRVAGSM 3651 bp ss-RNA VRL 03-AUG-1993
DEFINITION Sapporo rat virus mRNA M segment, encoding an ORF, complete cds.
ACCESSION M34882
VERSION M34882.1 GI:335017
KEYWORDS .
SOURCE Sapporo rat virus (strain SR-11), cDNA to viral RNA, passed in Vero E6 cell line C1008.

ORGANISM Sapporo rat virus
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.

REFERENCE 1 (bases 1 to 3651)
AUTHORS Arikawa, J., Lapenotiere, H.F., Iacono-Connors, L., Wang, M.G. and Schmaljohn, C.S.
TITLE Coding properties of the S and the M genome segments of Sapporo rat virus: Comparison to other causative agents of hemorrhagic fever with renal syndrome

JOURNAL Virology 176, 114-125 (1990)

MEDLINE 90232720

FEATURES
source Location/Qualifiers
1..3651
/organism="Sapporo rat virus"
/db_xref="taxon:11607"
47..3448

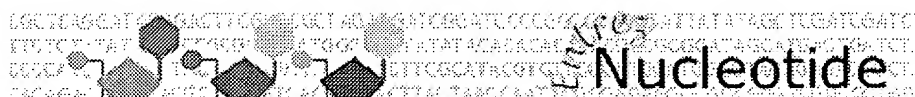
CDS
/note="M segment ORF"
/codon_start=1
/protein_id="AAA47825.1"
/db_xref="GI:335018"
/translation="MWSLLLLAALVGQGFALKNVFDMRIQLPHSVNFGETSVSGYTEF
PPLSLQEAELVPESSCNMDNHQSLSTINKLTKVIWRKKANQESANQNSFEVVESEVS
FKGLCMLKHRMVEESYRNRSSVICYDLACNSTFCKPTVYMIVPIHACNMMKSLIGLG
PYRIQVYERTYCTTGILTEGKCFVPDKAVVSALKRGMAYIASIETICFFIHQKNTY
KIVTAITSAMGSKCNNTDTKVQGYIICIIIGNSAPVYAPAGEDFRAMEVFSGIITSPH
GEDHDLPGEEIATYQISGQIEAKIPHTVSSKNLKLTAFAIGPSYSSTSILAASEDGRF
IFSPGLFPNLNQSVCDNNALPLIWRGLIDLTYGEEAVHPCNVFCVLSGPGASCEAFSE
GGIFNITSPMCLVSKQNRFRAAEQQISFVCQRVMDIIVYCNGQKKTILTKTLVIGQC
IYTITSLFSLLPVVAHSIAIELCVPGFHGWATAALLITFCFGWVLIIPACTLAILLVLK
FFANILHTSNQENRFKAILRKIKEEFKTKGSMVCEICKYECETLKEKLAHNLSVCVQG
ECPYCFTHCEPTETAIQAHYKVCQATHRFREDLKKTVTPQNIGPGCYRTLNLFRYKSR
CYILTMWTLILLIESILWAASAAEIPLVPLWTDNAHGVGSVPMHTDLELDFSLPSSSK
YTYKRHLTNPNVDQSVSLHIEIESQGIGAAVHHLGHWDARLNLKTSFHCYGACTKY
QYPWHTAKCHFEDKDYENSWACNPPDCPGVGTGCTACGLYLDQLKPVGTAFKIIISVR
YSRKVCVQFGEHLCKTIDMNDCFVTRHAKICIIIGTVSKFSQGDTLFLGPMEGGGII
FKHWCTSTCHFGDPGDVMPKDKPFICPEFPGQFRKKCNFATTPVCEYDGNIIISGYKK
VLATIDSFQSFNTSNIHFTDERIEWRDPDGMRLDHINIVISKDIDFENLAENPCKVGL
QAANIEGAWGSGVGFTLTCKVSLTECPTFLTSLIKACDMAICYGAESVTLRSGQNTVKI
TGKGGHSGSSFKCCHGKECSSTGLQASAPHLDKVNGISELENEKVYDDGAPECGITCW
FKKSGEWMGIINGNWVVLIVLCVLLLSLILLSILCPVRKHKKS"

BASE COUNT 1119 a 692 c 755 g 1085 t
ORIGIN

1 tagtagtaga ctccgcaaga aacagcagtt aaagaacaat aggatcatgt ggagtttget
61 attactggcc gcttttagttg gccaaaggctt tgcattaaaa aatgtatttg acatgagaat

```
121 tcagttgccc cactcagtc aactttgggga aacaagtgtg tcaggctata cagaatttcc
181 cccactctca ttacaggagg cagaacagct agtgccagag agctcatgca acatggacaa
241 ccaccagtca ctctcaacaa taaataaatt aaccaaggtc atatggcgga aaaaagcaaa
301 tcaggaatca gcaaaccaga attcatttga agttgtggaa agtgaagtca gctttaagg
361 gttgtgtatg ttaaagcata gaatggttga agaatacat agaaatagga gatcagtaat
421 ctgttatgat ctagcctgta atagtacatt ctgtaaacca actgtttata tgattgttcc
481 tatacatgct tgcaacatga tgaaaagctg tttgattggc cttggccctt acagaatcca
541 ggttgtctat gaaaggacat actgcactac gggatatatt acagaaggaa aatgctttgt
601 ccctgacaag gctgttgtca gtgcattgaa aagaggcatg tatgctatag caagcataga
661 gacaatctgc ttttttattc atcagaaagg gaatacatat aagatagtga ctgccattac
721 atcagcaatg ggctccaaat gtaataatag agatactaaa gttcaaggat attatatctg
781 tattattggt ggaaactccg cccctgtata tgccctgctt ggtgaagact tcagagcaat
841 ggagggtttt tctgggatta ttacatcacc acatggagaa gaccatgacc taccggcgga
901 agaaatcgca acgtaccaga tttcagggca gatagaggca aaaatccctc atacagttag
961 ctccaaaaac ttaaaattga ctgcttttgc aggtattcca tcatactcat caactagtat
1021 attggctgct tcagaagatg gtcgtttcat atttagtcct ggtttatttc ctaacctaaa
1081 tcagtcagtc tgtgacaaca atgcactccc tttaatctgg aggggacctt ttgatttaac
1141 gggatactat gaggcagtc acccttgcaa tgtgttctgt gtcttatcag gaccaggtgc
1201 ttcatgtgag gccttttcag aaggaggtat ttccaatatt acttctccaa tgtgtctggg
1261 gtctaagcaa aatagattta gagcagctga gcagcagatt agctttgtct gccaaagagt
1321 tgatatggat attatagtgt actgtaattg tcagaaaaaa acaatccata caaaaacatt
1381 agttataggc caatgtattt atactattac aagtctcttt tcaactgtac caggggttgc
1441 ccattctatt gctattgagt tgtgtgttcc agggtttcat ggctgggcca cagctgcact
1501 tttgattaca ttctgcttcg gctgggtatt gattcctgca tgtacattag ctattctttt
1561 agtccttaag ttctttgcaa atatccttca tacaagcaat caagagaacc gattcaaagc
1621 cattctacgg aaaataaagg aggagtttga aaaaacaaag ggttccatgg tttgtgagat
1681 ctgtaagtat gagtgtgaaa cattaaagga attgaaggca cataacctat catgtgttca
1741 aggagagtgc ccatattgct ttaccactg tgaaccgaca gaaactgcaa ttgaggcaca
1801 ttacaagatt gtcaagcca cccaccgatt cagagaagat ttaaaaaaga ctgtaactcc
1861 tcaaaatatt gggccaggct gttaccgaac actaaatctt tttaggata aaagtaggtg
1921 ttatattctg acaatgtgga ctcttcttct cattattgaa tccatcctct gggcagcaag
1981 tgcagcagaa atcccccttg tccctctctg gacagataat gctcatggcg ttgggagtgt
2041 tcctatgcat acggatcttg aattagactt ctctttgcca tccagttcta agtacacata
2101 caaaagacat ctcacaaacc cagttaatga ccaacagagt gtctcattgc atatagaaat
2161 tgaaagtcaa ggcattgggt ctgctgttca tcatcttgga cattgggatg atgcaagatt
2221 gaatctaaaa acctcatttc attgtttatg tgccctgcaca aaatatcaat acccatggca
2281 cactgcaaaa tgccattttg agaaagatta tgagtatgaa aatagctggg attgcaacct
2341 cccagattgc ccagggttg gtacaggttg tactgcttgt ggattatata tagatcaatt
2401 gaagccggtg ggaacagcct ttaaaattat aagtgtaga tacagttaga aagtgtgcgt
2461 gcagtttggg gaagaacacc tttgtaaaac aattgatatg aatgattgct ttgtgactag
2521 gcatgccaaa atatgtataa ttgggactgt atctaagttt tctcaaggtg acactctact
2581 atttctgggg cccatggaag gaggtggtat aatctttaa cactggtgta catctacctg
2641 tcactttgga gaccctggtg atgtcatggg tccaaaagat aaaccattta tttgccctga
2701 attcccaggg caatttagga aaaaatgtaa ctttgccaca actccagttt gtgaatatga
2761 tggaaacatt atatcaggct ataagaaagt acttgcaaca attgattctt tccaatcatt
2821 taacacaagc aatatacact tcactgatga gagaattgaa tggagagacc ctgatggcat
2881 gcttcgggat catattaata ttgttatttc taaagatatt gattttgaaa atttggctga
2941 gaatccttgt aaagtagggc tccaggcagc aaacatagaa ggtgcctggg gttcagggtg
3001 cgggtttaca ctcacatgca aggtgtctct cacagaatgc ccaacatttc ttacatcaat
3061 aaaggcctgt gacatggcaa tttgtttatg tgcagaaagt gtgacactct cacgaggaca
3121 aaatactgtc aaaattaccg ggaaagggtg ccatagtggg tcttcattca aatgctgtca
3181 tgggaaagaa tgttcatcaa ctggcctcca agccagtgc ccacatctgg ataaggtaaa
3241 tggatatctt gagttagaaa acgagaaagt ttatgatgac ggtgcacctg aatgtggcat
3301 tacttgttgg tttaaaaaat caggtgaatg ggttatgggt ataataatg ggaactgggt
3361 tctcctaatt gtcttgtgtg tactgtctgt ctttctctt atcctgttga gcatcttgtg
3421 tgctgttaga aagcataaaa aatcataaat cccacctaac aatcttcaca tcatgtatcg
3481 attttcaaac actttatcat ttagaactta acttggcact actatctgat aactgacttt
3541 catttttatt tttatatgga ttaattacta aaaaaaatac tctcttctat ctcccaatct
3601 tttattgatt caccgggggt ctgtcttgac atctggcggc gtctactact a
```

//



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search	Nucleotide	for					Go	Clear
Limits		Index		History		Clipboard		
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: **M34881 Sapporo rat virus mRNA S segment, encoding an ORF, complete cds** PubMed, Protein, Related Sequences, Taxonomy

LOCUS SRVAGSS 1769 bp ss-RNA VRL 03-AUG-1993
DEFINITION Sapporo rat virus mRNA S segment, encoding an ORF, complete cds.
ACCESSION M34881
VERSION M34881.1 GI:335019
KEYWORDS
SOURCE Sapporo rat virus (strain SR-11), cDNA to viral RNA, passed in Vero E6 cell line C1008.
ORGANISM Sapporo rat virus
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
REFERENCE 1 (bases 1 to 1769)
AUTHORS Arikawa, J., Lapenotiere, H.F., Iacono-Connors, L., Wang, M.G. and Schmaljohn, C.S.
TITLE Coding properties of the S and the M genome segments of Sapporo rat virus: Comparison to other causative agents of hemorrhagic fever with renal syndrome
JOURNAL Virology 176, 114-125 (1990)
MEDLINE 90232720
FEATURES
source Location/Qualifiers
1..1769
/organism="Sapporo rat virus"
/db_xref="taxon:11607"
CDS 43..1332
/note="S segment ORF"
/codon_start=1
/protein_id="AAA47826.1"
/db_xref="GI:335020"
/translation="MATMEEIQREISAHEGQLVIARQKVKDAEKQYKDPDDLNKRAL
HDRESVAASIQSKIDELKRQLADRLQQGRTSGQDRDPTGVEPGDHLKERSALSYGNTL
DLNSLDIDEPTGQTADWLTIIIVYLTFSFVVPILKALYMLTTRGRQTSKDNKGMRIREFK
DDSSYEDVNGIRKPKHLYVSMNPNAQSSMKAEIITPGRFRTAVCGLYPAQIKARNMVSP
VMSVVGFLALAKDWTSRIEEWLGAPCKFMAESLIAGSLSGNPNVDYIRQRQALAGM
EPKEFQALRQHSKDAGCTLVEHIESPSSIWVFAGAPDRCPPTCLFVGGMAELGAFFSI
LQDMRNTIMASKTVGTADEKLRKKSSFYQSYLRRTQSMGIQLDQRIIVFMFVAWGKEA
VDNFHLGDDMDPELRS LAQILIDQKVKEISNQEPMKL"
BASE COUNT 569 a 331 c 410 g 459 t
ORIGIN

```
1 tagtagtaga ctcctaag agctactaca ctaacaagaa aaatggcaac tatggaagaa
61 atccagagag aaatcagtgc tcacgagggg cagcttggtga tagcacgcca gaaggtcaag
121 gatgcagaaa agcagtatga gaaggatcct gaagacttaa acaagagggc actgcatgat
181 cgggagagtg tcgcagcttc aataacaatca aaaattgatg aattgaagcg ccaacttgcc
241 gacagattgc agcaggaag aacatccggg caggaccggg atcctacagg ggtagagcca
301 ggtgatcatc ttaaggaaag atcagcacta agctacggga atacactgga cctgaatagt
361 cttgacattg atgaacctac aggacagaca gctgattggc tgaccataat tgtctatctg
421 acatcattcg tgggtccgat catcttgaag gcactgtaca tgtaacaac acgaggtagg
481 cagacttcaa aggacaacaa ggggatgagg atcagattca aggatgacag ctcatatgag
541 gatgtcaatg gaatcagaaa gcccaaacat ctgtatgtgt caatgccaaa cgcccaatcc
601 agcatgaagg ctgaagagat aacaccagga agattccgca ctgcagtatg tggactatat
661 cctgcacaga taaaggcaag gaatatggta agcctgtgca tgagtgtagt tgggttcttg
721 gcactggcaa aagactggac atcagaaatt gaagaatggc tcggtgcacc ctgcaaatcc
781 atggcggagt ctcttattgc cgggagttta tctgggaatc ctgtgaatcg tgactatata
```

841 agacagagac aaggtgcact tgcagggatg gagccaaagg aatttcaagc cctcaggcaa
901 cattcaaagg atgctggatg tacactagtt gaacatattg agtcaccatc atcaatatgg
961 gtgtttgctg gggccctga taggtgtcca ccaacatgct tgtttgctcg agggatggct
1021 gaattagggtg ctttcttttc tatacttcag gatatgagga acacaatcat ggcttcaaaa
1081 actgtgggca cagctgatga aaagcttcga aagaaatcat cattctatca atcataacctc
1141 agacgcacac aatcaatggg aatacaactg gaccagagga taattgttat gtttatgggtt
1201 gcctggggaa aggaggcagt ggacaacttt catctcgggtg atgacatgga tccagagctt
1261 cgtagcctgg ctcatgctt gattgaccag aaagtgaagg aaatctcaaa ccaggaacct
1321 atgaaattat aagtacataa atatataatc aatactaact atagggttaag aaataactaat
1381 cattagttaa taagaatata gatttattga ataatacat taaataatta ggtaagttaa
1441 ctagtattta gtttaagttag ctaattgatt tatatgattg tcacaattaa atgtaatcat
1501 aagcacaatc actgccatgt ataatacagg gtatacgggt ggttttcata tggggaacag
1561 ggtgggctta gggccaggtc accttaagt accttttttt gtatatatgg atgtagattt
1621 caattgatcg aatactaata ctactgtcct cttttctttt cttttctcct tctttactaa
1681 caacaacaaa ctacctaca ccttaatata tactacttta ttaagttggt aagttgtgtc
1741 tttttgggga gtaaggaggt ctactacta

//

[Restrictions on Use](#) | [Write to the HelpDesk](#)
[NCBI](#) | [NLM](#) | [NIH](#)